

REMARKS

Applicants respectfully request entry of the amendments and remarks submitted herein. Claims 1-9, 14-15, and 18-30 have been canceled. Claim 10 has been amended herein, and new claims 31-40 have been added. Therefore, claims 10-13, 16-17 and 31-40 are currently pending. Attached is a marked-up version of the changes being made by the current amendments. Reconsideration of the pending application is respectfully requested.

Applicants submit herewith a paper copy of the Sequence Listing and a request to transfer the computer readable form of the Sequence Listing from the parent application to the present application. Applicants have amended the specification to include appropriate sequence identifiers. Applicants have further amended the specification to correct obvious typographical errors. No new matter is introduced by these amendments.

CONCLUSION

Applicant asks that pending claims 10-13, 16-17, and 31-40 be examined. The filing fee enclosed reflects the claim amendments herein. Please apply any charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date: June 18, 2001

M. Angela Parsons  
M. Angela Parsons, Ph.D.  
Reg. No. 44,282

Fish & Richardson P.C., P.A.  
60 South Sixth Street  
Suite 3300  
Minneapolis, MN 55402  
Telephone: (612) 335-5070  
Facsimile: (612) 288-9696  
60043601.doc

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The paragraph bridging pages 7 and 8 has been amended as follows:

In some embodiments, a polynucleotide of the invention encodes analogs or derivatives of a polypeptide having the deduced amino acid sequence of Figs. 4, 6, 8, 10, 12, 14 or 16. Such fragments, analogs[ on] or derivatives include, for example, naturally occurring allelic variants, non-naturally occurring allelic variants, deletion variants and insertion variants, that do not substantially alter the function of the polypeptide.

The paragraph on page 12, lines 16-22 has been amended as follows:

A nucleic acid construct of the invention comprises a polynucleotide as disclosed herein linked to another, different polynucleotide. For example, a full-length KAS coding sequence may be operably fused in-frame to a nucleic acid fragment that encodes a leader sequence, secretory sequence or other additional amino acid sequences that[ amy] may be usefully linked to a polypeptide or peptide fragment.

The paragraph on page 13, lines 18-23 has been amended as follows:

One may use a polynucleotide disclosed herein for cosuppression as well as for antisense inhibition. Cosuppression of genes in plants may be achieved by expressing, in the sense orientation, the entire or partial coding sequence of a gene. See, e.g., WO 94/11516 [04\11516], incorporated herein by reference.

The paragraph on page 17, lines 8-14 has been amended as follows:

The open reading frame of the *Arabidopsis FAE1* gene was amplified directly by PCR, using *Arabidopsis thaliana* cv. Columbia genomic DNA as a template, pfu DNA polymerase and the following primers: 5'-CTCGAGGAGCAATGACGTCCGTAA-3' and 5'-CTCGAGTTAGGACCGACCGTTTGTG-3' (SEQ ID NOS:15 and 16, respectively). The PCR product was blunt-end cloned into the *Eco* RV site of pBluescript (Stratagene, La Jolla, CA).<sub>2</sub>[.]

The paragraph on page 28, lines 3-13 has been amended as follows:

The open reading frames (ORFs) for the EL2, EL4 and EL7 clones were amplified by PCR. The EL2 ORF was cloned into  $\lambda$ YES using the primers: CTCGAGCAAGTCCACTACCAACGCA and CTCGAGCGAGTCAGAAGGAACAAA (SEQ ID NOS:17 and 18, respectively). The EL4 ORF was cloned into pYEUra3 using the primers: GATAATTTAGAGAGGCACAGGGT and GTCGACACAAGAATGGGTAGATCCAA (SEQ ID NO:19 and 20, respectively). The EL7 ORF was cloned into pYEUra3 using the primers: CAGTTCCTCAAACGAAGCTA and GTCGACTTCTCAATGGACGGTGCCGGA (SEQ ID NOS:21 and 22, respectively). Amplified products were cloned into pYEUra3 under the control of, and 3' to, the GAL1 promoter. The resulting plasmids were transformed into yeast as described in Example 1.

In the Claims:

Claims 1-9, 14-15, and 18-30 have been cancelled.

Claim 10 has been amended as follows:

10. (Amended) An isolated polypeptide [having an amino acid sequence] selected from the group consisting of: [an amino acid sequence substantially identical] a polypeptide having at least 80% sequence identity to SEQ ID NO:2, [an amino acid sequence substantially identical] a polypeptide having at least 80% sequence identity to SEQ ID NO:4, [an amino acid sequence substantially identical] a polypeptide having at least 80% sequence identity to SEQ ID NO:6, [an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical] a polypeptide having at least 80% sequence identity to SEQ ID NO:12, and [an amino acid sequence substantially identical] a polypeptide having at least 80% sequence identity to SEQ ID NO:14.

The following new claims have been added.

31. An isolated polypeptide having the amino acid sequence of SEQ ID NO:8.

32. An isolated polypeptide having the amino acid sequence of SEQ ID NO:10.
33. A transgenic plant containing a nucleic acid that encodes a polypeptide selected from the group consisting of: a polypeptide having at least 80% sequence identity to SEQ ID NO:2, a polypeptide having at least 80% sequence identity to SEQ ID NO:4, a polypeptide having at least 80% sequence identity to SEQ ID NO:6, a polypeptide having at least 80% sequence identity to SEQ ID NO:12, and a polypeptide having at least 80% sequence identity to SEQ ID NO:14.
34. The plant of claim 33, wherein expression of said nucleic acid is tissue-specific.
35. The plant of claim 34, wherein said expression is epidermal cell-specific expression.
36. The plant of claim 34, wherein said expression is seed-specific expression.
37. The plant of claim 33, wherein said plant has altered levels of very long chain fatty acids in seeds compared to the levels in a plant lacking expression of said nucleic acid.
38. A transgenic plant containing a nucleic acid that encodes a polypeptide having the amino acid sequence of SEQ ID NO:8.
39. A transgenic plant containing a nucleic acid that encodes a polypeptide having the amino acid sequence of SEQ ID NO:10.
40. A method of altering the levels of very long chain fatty acids in a plant, comprising the step of:  
introducing a nucleic acid construct into a plant, wherein said nucleic acid construct encodes a polypeptide selected from the group consisting of: a polypeptide having at

least 80% sequence identity to SEQ ID NO:2, a polypeptide having at least 80% sequence identity to SEQ ID NO:4, a polypeptide having at least 80% sequence identity to SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, a polypeptide having at least 80% sequence identity to SEQ ID NO:12, and a polypeptide having at least 80% sequence identity to SEQ ID NO:14, wherein said construct is expressed and wherein said polypeptide is effective for altering the levels of very long chain fatty acids in said plant.

Symbol	Definition	Symbol	Definition
$\mathcal{A}$	Algebra	$\mathcal{B}$	Algebra
$\mathcal{C}$	Algebra	$\mathcal{D}$	Algebra
$\mathcal{E}$	Algebra	$\mathcal{F}$	Algebra
$\mathcal{G}$	Algebra	$\mathcal{H}$	Algebra
$\mathcal{I}$	Algebra	$\mathcal{J}$	Algebra
$\mathcal{K}$	Algebra	$\mathcal{L}$	Algebra
$\mathcal{M}$	Algebra	$\mathcal{N}$	Algebra
$\mathcal{O}$	Algebra	$\mathcal{P}$	Algebra
$\mathcal{Q}$	Algebra	$\mathcal{R}$	Algebra
$\mathcal{S}$	Algebra	$\mathcal{T}$	Algebra
$\mathcal{U}$	Algebra	$\mathcal{V}$	Algebra
$\mathcal{W}$	Algebra	$\mathcal{X}$	Algebra
$\mathcal{Y}$	Algebra	$\mathcal{Z}$	Algebra
$\mathcal{A}_1$	Algebra	$\mathcal{A}_2$	Algebra
$\mathcal{A}_3$	Algebra	$\mathcal{A}_4$	Algebra
$\mathcal{A}_5$	Algebra	$\mathcal{A}_6$	Algebra
$\mathcal{A}_7$	Algebra	$\mathcal{A}_8$	Algebra
$\mathcal{A}_9$	Algebra	$\mathcal{A}_{10}$	Algebra
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